AMENDMENT TO THE CLAIMS

1. (Withdrawn) An isolated polypeptide selected from the group consisting of:

(a) a polypeptide comprising at least 223 contiguous amino acids of an hPNQALRE protein selected from the group consisting of SEQ ID NO:4, SEQ ID NO:6 and SEQ ID NO:8;

(b) a polypeptide comprising an amino acid sequence that is at least 65% identical to amino acids 26-38 of SEQ ID NO:6;

(c) a polypeptide comprising an amino acid sequence identical to amino acids 26-38 of SEQ ID NO:6;

(d) a polypeptide comprising an amino acid sequence that is at least 65% identical to amino acids 181-201 of SEQ ID NO:6;

(e) a polypeptide comprising an amino acid sequence identical to amino acids 181-201 of SEQ ID NO:6; and

(f) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, and SEQ ID NO:8.

2. (Withdrawn) The isolated polypeptide of claim 1 comprising an amino acid sequence that is at least 65% identical to amino acids 26-38 of SEQ ID NO:6.

3. (Withdrawn) The isolated polypeptide of claim 1 comprising an amino acid sequence that is at least 65% identical to amino acids 181-201 of SEQ ID NO:6.

4. (Withdrawn) A fusion protein comprising a first protein segment and a second protein segment wherein said first protein segment is fused to said second protein segment by means of a peptide bond and wherein said first protein segment comprises an isolated polypeptide of claim 1.

5. (Withdrawn) A preparation of antibodies that specifically bind to an epitope defined in whole or in part by an isolated polypeptide of claim 1.

6. (Withdrawn) A cDNA molecule that encodes the isolated polypeptide of claim 1.

7. (Withdrawn) A cDNA molecule that encodes the isolated polypeptide of claim 2.

8. (Withdrawn) A cDNA molecule that encodes the isolated polypeptide of claim 3.

9. (Withdrawn) A cDNA molecule comprising a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence that is at least 65% identical to nucleotides 76-114 of SEQ ID NO:5;

(b) a nucleotide sequence that is identical to nucleotides 76-114 of SEQ ID NO:5;

(c) a nucleotide sequence that is at least 65% identical to nucleotides 503-564 of SEQ ID NO:3 or to nucleotides 542-603 of SEQ ID NO:5;

(d) a nucleotide sequence that is identical to nucleotides 503-564 of SEQ ID NO:3 or to nucleotides 542-603 of SEQ ID NO:5; and

(e) a nucleotide sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5 and SEQ ID NO:7.

10. (Withdrawn) An isolated subgenomic polynucleotide or the complement thereof comprising a nucleotide sequence that hybridizes under stringent conditions to a nucleotide sequence selected from the group consisting of nucleotides 76-114 of SEQ ID NO:5 and nucleotides 503-564 of SEQ ID NO:3.

11. (Withdrawn) A construct comprising:

a promoter; and

a polynucleotide segment comprising a cDNA of claim 6, wherein said polynucleotide segment is located downstream from said promoter and wherein transcription of said polynucleotide segment initiates at the promoter.

12. (Withdrawn) A construct comprising:

a promoter; and

a polynucleotide segment comprising a cDNA of claim 9, wherein said polynucleotide segment is located downstream from said promoter and wherein transcription of said polynucleotide segment initiates at the promoter.

13. (Withdrawn) A host cell comprising the construct of claim 11.

14. (Withdrawn) A host cell comprising the construct of claim 12.

15. (Withdrawn) A homologously recombinant cell having incorporated therein a new transcription initiation unit, wherein said new transcription initiation unit comprises:

(a) an exogenous regulatory sequence;

(b) an exogenous exon; and

(c) a splice donor site, wherein the new transcription initiation unit is located upstream of a coding sequence of a gene, wherein said gene has a coding sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5 and SEQ ID NO:7 and wherein said exogenous regulatory sequence directs transcription of the coding sequence of the gene.

16. (Currently Amended) A method of ~~diagnosing or prognosing neoplasia~~ determining if a cell is neoplastic, comprising the step of comparing expression of a first *hPNQALRE* gene in a first ~~tissue~~ cell suspected of being neoplastic with expression of a second *hPNQALRE* gene in a second ~~tissue~~ cell which is normal, wherein said first and said second *hPNQALRE* genes comprise a coding sequence selected from the group consisting of:

(a) SEQ ID NO:1;

(b) SEQ ID NO:3;

(c) SEQ ID NO:5;

(d) SEQ ID NO:7;

(e) nucleotides 76-114 of SEQ ID NO:5;

(f) nucleotides 503-564 of SEQ ID NO:3; and

(g) nucleotides 542-603 of SEQ ID NO:5, wherein over-expression of said first *hPNQALRE* gene in said first ~~tissue~~ cell indicates neoplasia in said first ~~tissue~~cell.

17. (New) The method of claims 16 wherein said first cell is a lung cancer cell.

18. (New) The method of claims 16 wherein said first cell is an epithelial cancer cell.

19. (New) The method of claims 16 wherein said first cell is a colon cancer cell.